Amendments to the Specification:

Please amend page 3, lines 28-30 as follows:

Figure 5 shows a multiple protein sequence alignment between the predicted amino acid sequences of NBS1 (SEQ ID NO:2), NBS2 (SEQ ID NO:4), NBS4 (SEQ ID NO:8), NBS6 (SEQ ID NO:12) and the cloned blast resistance gene Pib (SEQ ID NO:16).

Please amend page 19, lines 9-31 and page 20, lines 1-4 as follows:

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Such implementations include, but are not limited to: CLUSTAL in the PC/Gene program (available from Intelligenetics, Mountain View, California); the ALIGN program (Version 2.0) and GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Version 8 (available from Genetics Computer Group (GCG), 575 Science Drive, Madison, Wisconsin, USA). Alignments using these programs can be performed using the default parameters. The CLUSTAL program is well described by Higgins *et al.* (1988) *Gene* 73:237-244 (1988); Higgins *et al.* (1989) *CABIOS* 5:151-153; Corpet *et al.* (1988) *Nucleic Acids Res.* 16:10881-90; Huang *et al.* (1992) *CABIOS* 8:155-65; and Pearson *et al.* (1994) *Meth. Mol. Biol.* 24:307-331. The ALIGN program is based on the algorithm of Myers and Miller (1988) *supra*. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. The BLAST programs of Altschul *et al* (1990) *J. Mol. Biol.* 215:403 are based on the algorithm of Karlin and Altschul (1990) *supra*. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding a protein of the invention. BLAST protein searches can be performed with the BLASTX program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a protein or polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST (in BLAST 2.0) can be

utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389. Alternatively, PSI-BLAST (in BLAST 2.0) can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, PSI-BLAST, the default parameters of the respective programs (e.g., BLASTN for nucleotide sequences, BLASTX for proteins) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~ Alignment may also be performed manually by inspection.

Please amend page 36, lines 3-18 as follows:

Five pairs of primers (RG64 [431: SEQ ID NO:17 and 432: SEQ ID NO:18], NBS1 [pi9-p5: SEQ ID NO:19 and pi9-p6: SEQ ID NO:20], NBS2 [pi9-p9: SEQ ID NO:21 and pi9-pi10: SEQ ID NO:22], NBS4 [NBS6F1: SEQ ID NO:23 and NBS4 pi9-p12: SEQ ID NO:24, and NBS6) (Table 1) were designed based on the genomic sequence at the Pi9 region. These primers were first used to screen for polymorphism between C101A51 and CO39. NBS1 and NBS6 primers could not amplify a specific band from CO39 whereas NBS2 primers could only amplify a specific band from C101A51. NBS4 primers amplified bands from both C101A51 and CO39, but with different sizes of PCR product. For RG64 primers, a polymorphism was observed between the two parents only after digestion of the PCR product with the restriction enzyme *Hae*III (Hittalmani *et al.* (1995) *Theor. Appl. Genet.* 100:1121-1128). Thus, we used NBS2, NBS4, and RG64 primers to screen a total of 505 susceptible plants. Fifteen recombinants were found at the RG64 locus, which is consistent with the RFLP mapping results of a 2.8 cM distance between the marker and the Pi2 gene (Yu *et al.* (1991) *Theor. Appl. Genet.* 81:471-476). Eight recombinants were identified in another 426 F2 plants between the RFLP marker R2131, indicating a distance of 2.7 cM from the Pi2 gene. No recombinants were found between Pi2 and either the NBS2 or NBS4 marker in the 505 susceptible plants. These results indicate that Pi2 is highly linked to both NBS2 and NBS4.

Please replace Table 3 on page 40 as follows:

Table 3. Primer sequence used in cloning cDNA of *NBS2* and *NBS4*

BAC84F1	TTG AAA GCG AAG AAG ACA TT	SEQ ID NO:25
BAC84R1	GAC GAC CAC ATT TAT TTA CA	SEQ ID NO:26
NBS2-p1	AAC GAA TCC ATG GCG GAG AC	SEQ ID NO:27
NBS2-p2	TGA TAT CAT GAA TTC GAC AAG	SEQ ID NO:28
NBS2-p3	AGT TCA GGA AAA CAC TCG CC	SEQ ID NO:29
NBS2-p4	CCA TAC CTG TTT TGC AGG AC	SEQ ID NO:30
NBS2-p5	GGA GCA TTA TTC GAT CAT TAG	SEQ ID NO:31

Please amend table 4 on page 41 as follows:

Table 4. Primer sequence for analysis of the mutant lines of C101A51

Locus	Name	Sequence	
Nip	pi9-p4	CAC TGA ATA ACG ACT ACA TC	SEQ ID NO:32
	pi9-p15	ATT GGT GGT TGG GCA TCT AG	SEQ ID NO:33
Nbs2	pi9-p9	TCT ATA GAA GTG CAA ACA GC	SEQ ID NO:34
	pi9-p10	TTA GGT ACG AAC ATG AGT AG	SEQ ID NO:35
BAC6F	BAC6F-1	TCA TTA AGA TTA AGG AGC CC	SEQ ID NO:36
	BAC6F-2	CAT GGT TGC TAT ATT TTA GG	SEQ ID NO:37
Nbs1	NBS-LRR-F2	CAC TGT TGT AGC GGA GGA GA	SEQ ID NO:38
	pi2-p2	TTC GAT GGC GTT CAC CAA G	SEQ ID NO:39
Nbs2-5'	pi2-p8	CCA ATG TCT GCA TAC TCT TC	SEQ ID NO:40
	pi2-p5	ATT CCA ACC TGC AGC AAG AG	SEQ ID NO:41
Nbs2-3'	BAC84F	TTG AAA GCG AAG AAG ACA TT	SEQ ID NO:42
	pi2-p5	GGA GCA TTA TTC GAT CAT TAG	SEQ ID NO:43